

FIG. 1

r ARMS	MSVLISQSVINYVEEENIPALKALLEKCKDVERNECGQTPMLAAEQGNVEIVKELLKNGANCNLEDLD	70
h ARMS	I L I	70
r ARMS	NWTALISASKEGHIHIVEELLKSGASLEHRDMGGWTALMWACYKGRTDVVELLLSHGANPSVTGLQYSVY	140
h ARMS	V C VN	140
r ARMS	PITWAAGRGHADIVHLLQNGAKVNCSDKYGTPLVWAARKGHECVKHLLANGADVQEGANSMTALIV	210
h ARMS		210
r ARMS	AVKGGYTQSVKEILKRNPVNLTDKDGNTALMIASKEGHIEIVQDLLDAGTYVNI PDRSGDTVIGAVRG	280
h ARMS	T	280
r ARMS	GHVEIVRALLQKYADIDIRGQDNKTALYWAVEKGNATMVRDILQCNPDTEICTKDGETPLIKATKMRNIE	350
h ARMS		350
r ARMS	VVELLLDKGAKVSAVDKKGDTPLHVAIRGRSRRLAELLRNPKDGRLLYRPNKAGETPYNIDCSHQKSIL	420
h ARMS	I K	420
r ARMS	TQIFGARHLSPTETDGM LGYDLYSSALADILSEPTMQPPICVGLYAQWGS GKSFLKKLEDEMKT FAGQ	490
h ARMS		490
r ARMS	QTEPIFQFSWLIVFLTLLCGGLGLVFAPVDTNLALAIISLSFLALIYIFFIVYFGRREGESWNWAWA	560
h ARMS	I L T HP G V L V	560
r ARMS	LSTRLARHIGYLELLFKLMFVNPPPEQTTKALPVRFLFTDYNRLSSVGGETSLAEMIATLSDACEREF	630
h ARMS	L	630
r ARMS	GFLATRLFRVFRTEESQGGKKWKKTCLPSFVIFLFI VGCIIAGITLLAIFRVDPKHITVNAILISIASV	700
h ARMS	K DT I S V	700
r ARMS	VGLAFVLNCR TWQVLDSSLNSQRKRLHSAASKLHLKSEGFMKVLKCEVELMARMAKTIDSFTQNQTRL	770
h ARMS	N	770
r ARMS	VVIIDGLDACEQDKVLQMLDTVRVLSKGPFI AIFASDPHIIKAINQNLNSVLRDSNINGHDYMRNIVH	840
h ARMS		840
r ARMS	LPVFLNSRGLSNARKFLVTSATNGDITCSDTTGTQEDTDRRVSONSLGEMTKLGSKTALNRRD TYRRRQM	910
h ARMS	VP I A	910
r ARMS	QRTITRQMSFDLTKLLVTEDWFSDISPQTMRRLLNIVSVTGRLLRANQITFNWDRLASWINLTEQWPYRT	980
h ARMS	S	980
r ARMS	SWLILYLEETEGLPDQMTLKTMYERISKNIPTTKDVEPLLEIDGDIRNFEVFLSSRTPVLVARDVKTF LFP	1050
h ARMS	I I V	1050
r ARMS	CTVNLDPKLREIIADVRAAREQINIGGLAY PPLPLHEGPPRPPSGYSQPASVCSSASFNGPFGGVVSPQ	1120
h ARMS	S A P T A	1120
r ARMS	PHSSYYSGLSGPQHFPYNRAAVPATGSSLLSSMTVDV VCEKLRQIEGLDQNMMPQYCTTIKKANINGRV	1190
h ARMS	MT GSG P PVV N LN A K S L	1190
r ARMS	LSQCNI DELKKEMAMNFGDWHLFRSMVLEMR SVESQVVPEDPRFLNENSSAPVPHGESARRSSHTELPLT	1260
h ARMS	A N T NA H S S G A P A N H	1260
r ARMS	ELSSQTPYTLNFSFEELNTLGLDEGAPRHSNLSWSQSTRRTPSLSSLSQDSSIEISKLTDKVQAEYRDA	1330
h ARMS		1330
r ARMS	YREYIAQMSQLEGGTGSSTISGRSSPHSTYYIGQSSSGGSIHSTLEQERGKEGELKQEDGRKSFLMKRGD	1400
h ARMS	P T M N K DS P PD	1400
r ARMS	VIDYSSSGVSTNEASPLDPITEEDEKSDQSGSKLLPGKKSSERPSLFQTDLKLKGGGLRYQKLPSDEDES	1470
h ARMS	D S S	1470
r ARMS	GTGRVQITPHCSKMIRTKRLKAKQRECA SPQEHSAEPIRTFIKAEYLSDALLDKXSSDSGVRSSNESSP	1540
h ARMS	EESDN LLKDDKDR AEGKVE VPK S	1539
r ARMS	NHSLHNEAADD SQLEKANLIELEDEGHSGKRGMPHSLSGLDPIIARMSICSEDKKS PSECSLIASSPEE	1610
h ARMS	V DS I	1609
r ARMS	SWPACQKAYNLNRT PSTVTLNNTAPTNRANQNFDEIEGIRETSQVILRPGPSPNP TAVQNNENLKSMAHK	1680
h ARMS	N S A M SS TI T	1679
r ARMS	RSQRSSYTRLSKDASELHAASS-ESTGFGEERESIL	1715
h ARMS	PP A S *** 1715	

FIG. 2

[illegible]

2. Loop between H12 and H13			
rARMS	573	ELLFKLMFVNPPPELPEQTTKALPVRFLFTDYNRLSSVGGETSLAEMIATLSDACEREFGFLATRLF	638
hARMS	573	ELLLKLMFVNPPPELPEQTTKALPVRFLFTDYNRLSSVGGETSLAEMIATLSDACEREFGFLATRLF	638
dARMS	594	RLILQVAFCHPP-GPQSDSQAKPVRFHFAEANSASPTG-DGAVAHMLAALLDAIESHYGWLATRLY	657
wARMS	565	RLVYNILTLHAP-MNSEDSASMPVSFLFADYHRLSSIGGEQALAKIVATLFEAAETHFGVLPVRLF	629

```
rARMS      749  EVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDKVLQMLDTRVRLFSK---GPFIAIFASDPHIIKA
hARMS      749  EVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDKVLQMLDTRVRLFSK---GPFIAIFASDPHIIKA
dARMS      740  EVAVMMDMKVKCLDAFTNQSRSLVGVIDALDCDETRITLLNNAVQTLLSS-PNRPFVLLISVDPHVIAKA
wARMS      769  EVDLLADMIRSLDAFTRSHRTLVRVVVDGLDNCEQERMVQTLDALELLFSARKHRPFTIIVADPHVISA
          **   ::  *   :  :*:*...::**  :*. ** *  ::::  *:..  .*:  ***:  ::  ***.*  .*
```

```
rARMS      INQNLNSVLRDSNINGHDYMRNIHVLPVFLNSRGLSNAR    854
hARMS      INQNLNSVLRDSNINGHDYMRNIHVLPVFLNSRGLSNAR    854
dARMS      AEANSRRLFTEGGIGGHDFLRNLVHLPVYLQNSGLRKVQ    848
wARMS      INHNMHSAISGTELTHGDYLNKIISMFPFYLHNSALRQLQ    876
          *   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
```

```

rARMS      940  MRRLLNIIVSVTGRLLLRANQITFNWDRLASWINLTEQWPYRTSWLILYLEETEETG--LPDQMTLKTMYERIS
hARMS      940  MRRLLNIIVSVTGRLLLRANQISFNWDRLASWINLTEQWPYRTSWLILYLEETEETG--IPDQMTLKTMYERIS
dARMS      980  MRRMNVNIYITVRLMKAFQIEFSWYRLSSWINLTEQWPLRASMIVLHHDQFMDSDNADESVSLSQSVYEKLR
wARMS      923  MRRIVNALTLTRLLMRAFEIDFSWMSLGHVWSLLEQWPLSRMCWLIDRALEVHN---NQLLLSVYYQLK
          ***::*: : * **::* : * * * * . *::* **** * : : : : : : : * : :
rARMS      KNIPTTKDVEPLLEIDGDIRNFEVFLSSR----TPVLVARDVKTFPLPCTVNLDPKLR 1060
hARMS      KNIPTTKDVEPLLEIDGDIRNFEVFLSSR----TPVLVARDVKVFLPCTVNLDPKLR 1060
dARMS      PKLAYLREAAPLLELDRDRERKLDAFLQLH----KSDLLVADRIFLPFTINLDPYLR 1102
wARMS      DHIP---AQDDLMQLDRNLENFEGFLDSKGIPSAERLTGVGHVKKFVPCSTSLDPYLR 1042
          : : : : : * : : : : * : : : : * : : : : * : : : : * : : : :

```

rARMS	1151	LSSMTVDVVCEKLRQIEGLDQNMMPQYCTTIKKANINGRVLSQCNI	DELKKEMAMNFGDWHLFR	1214
hARMS	1151	LNSLNVDVACEKLRQIEGLDQSMPLQYCTTIKKANINGRVLAQCNI	DELKKEMNMNFGDWHLFR	1214
dARMS	1193	LTDLTVEGVISLLDRIEDMKP-ALPKLAPVURENAINGRVLKHC	MDPLKSVLGLSFGHWELFR	1255
wARMS	1087	LVMKMLDAVVNLIRKIDIPSN-RLDSILDRFYQLNCLGLVLATC	PLPELKDSMQLPLGDWTLIR	1149
		* * * * *	* * * * *	

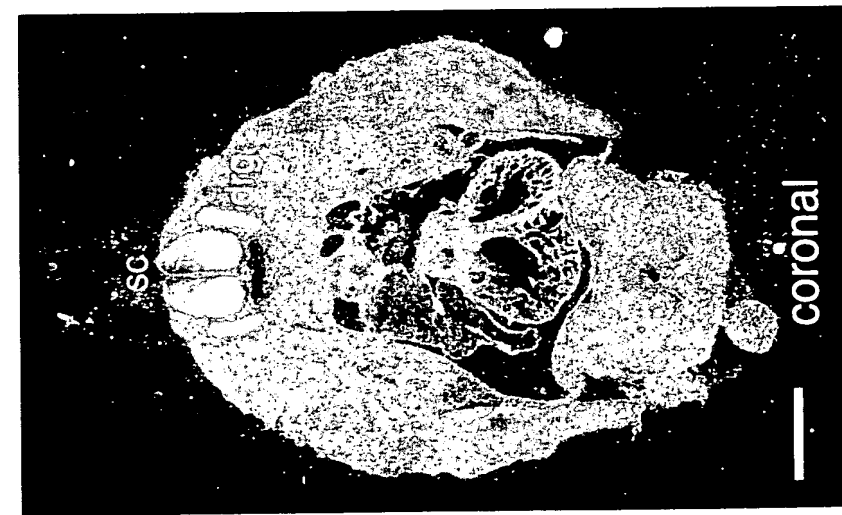


FIG. 7A

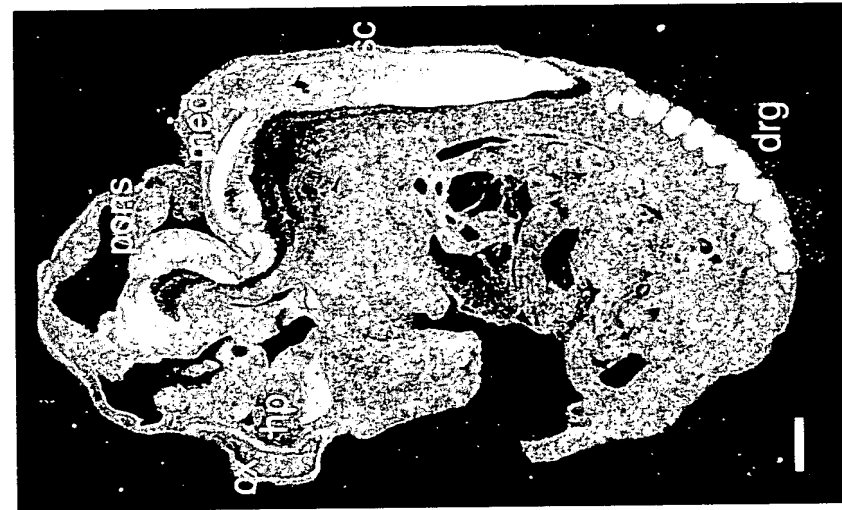
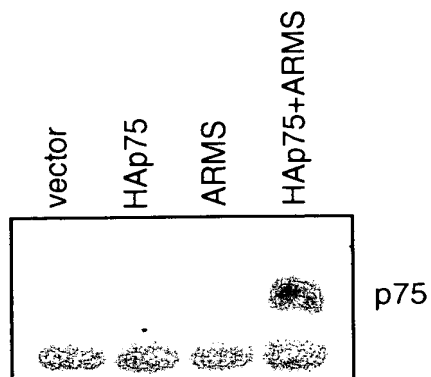


FIG. 7B



FIG. 7C

IP: 892
BLOT: HA



p75

FIG. 8B

LYSATES
BLOT: 9992

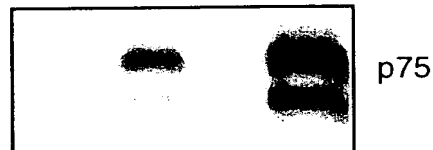


FIG. 9A

NGF: 0 10m 25h 25h

217 —

ARMS

IP: C14 IgG

217 —

← ARMS

IP: C14 IgG



FIG. 9B

FIG. 9C

FIG. 9D

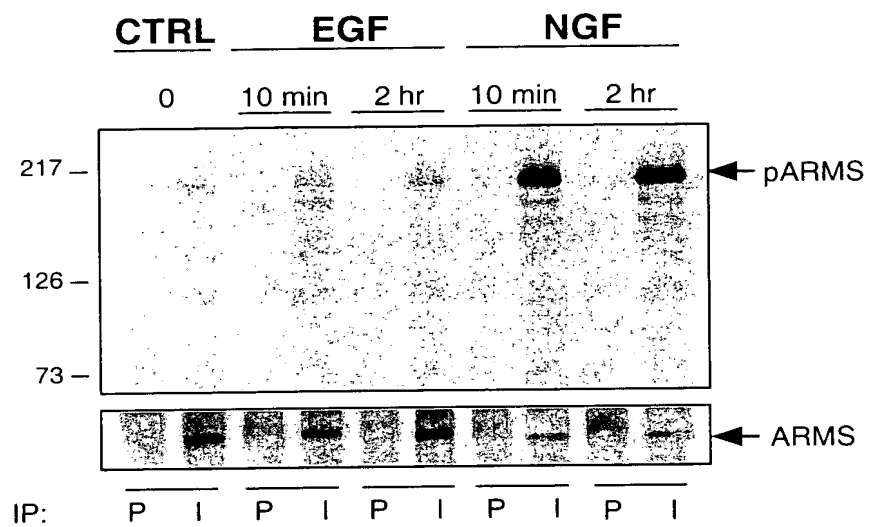
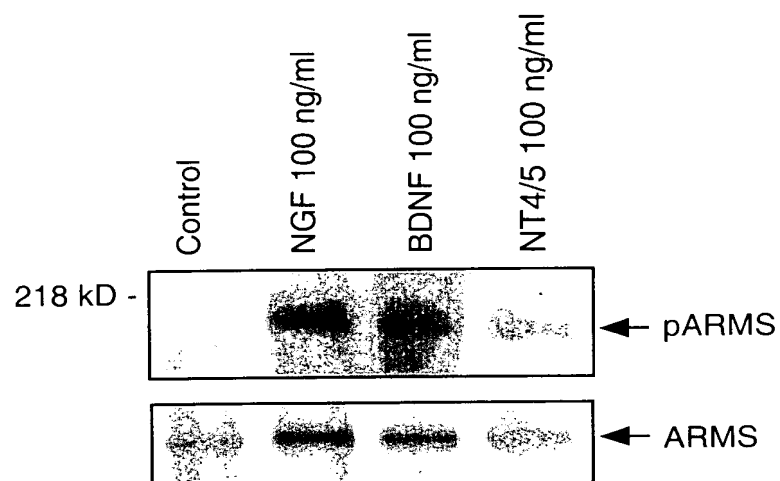


FIG. 11



IP: 892

FIG. 12

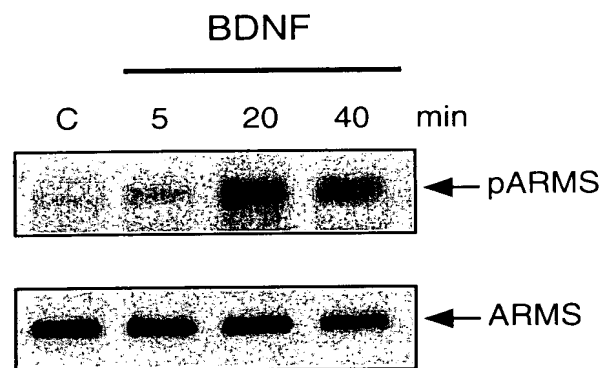


FIG. 13

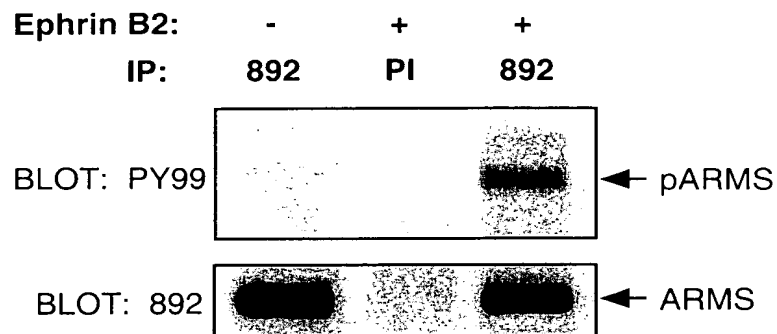


FIG. 14A

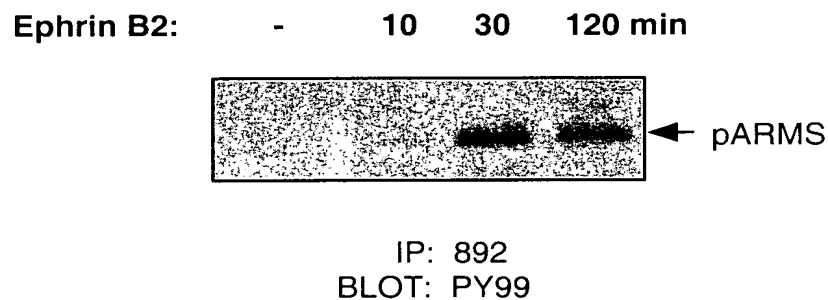


FIG. 14B

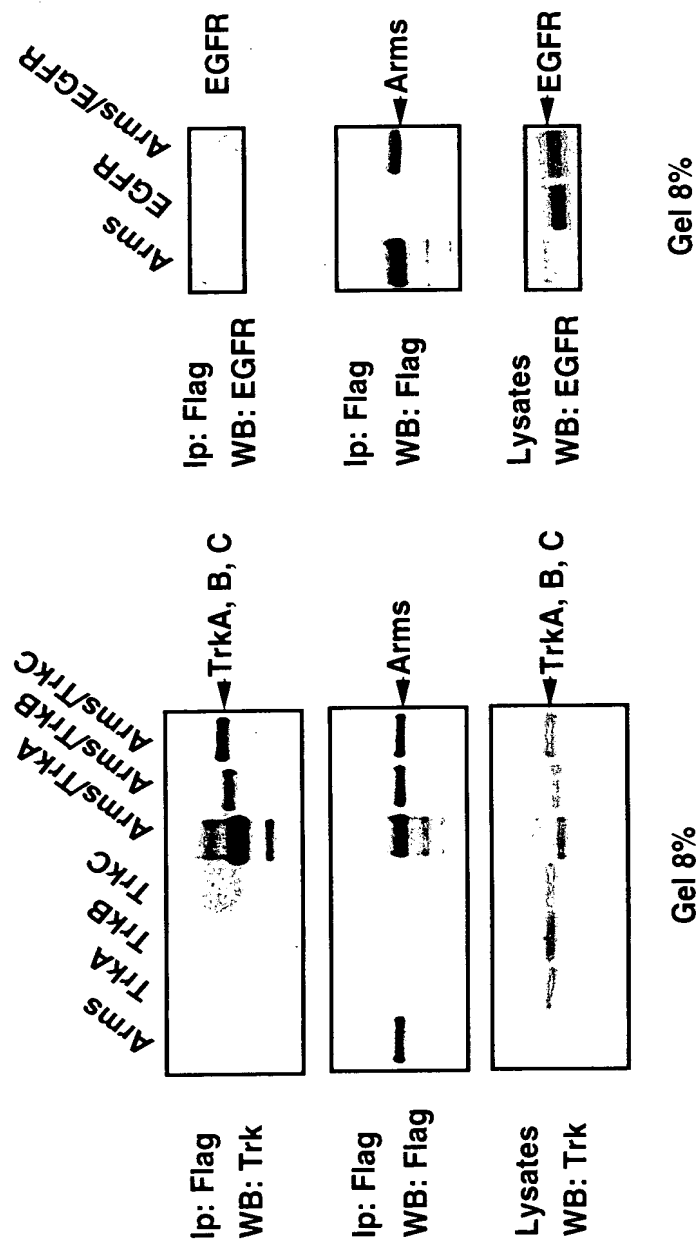


FIG. 15A

FIG. 15B

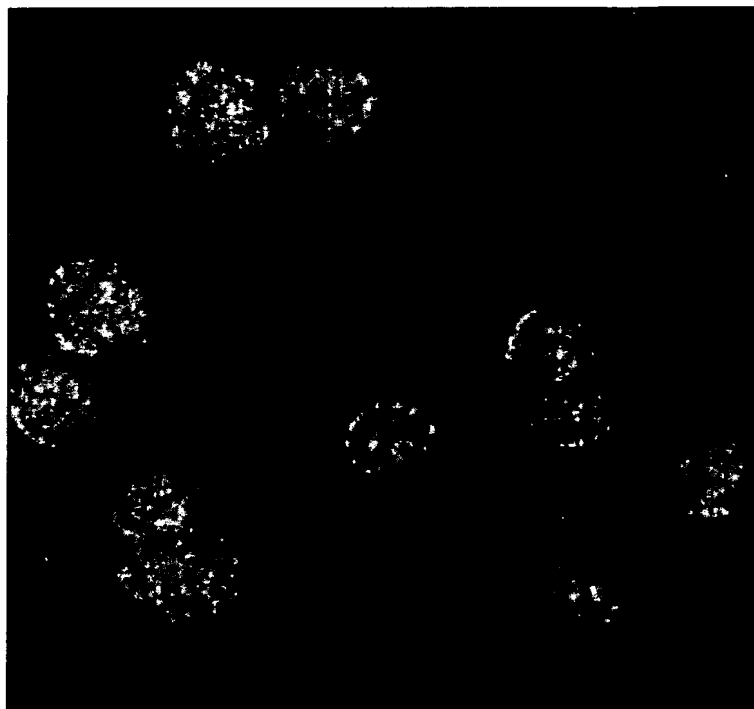


FIG. 16A

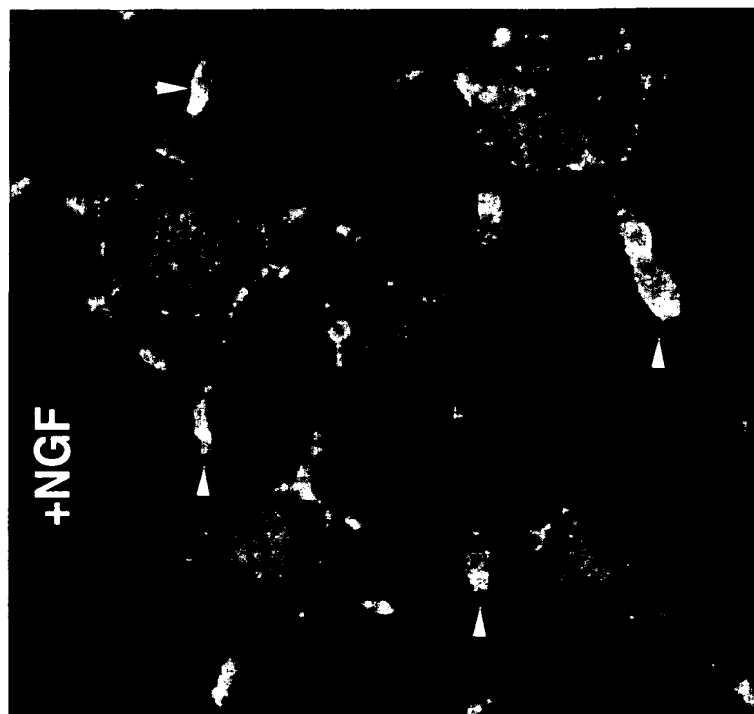
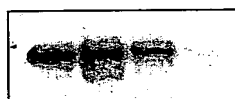


FIG. 16B

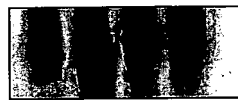
FIG. 18

Myc-GRIP 1	+	-	-	-
Myc-GRIP 2	-	+	-	-
Myc-PICK1	-	-	+	-
ARMS	+	+	+	+

WB: α ARMS



- ARMS



- ARMS

lysates

FIG.19

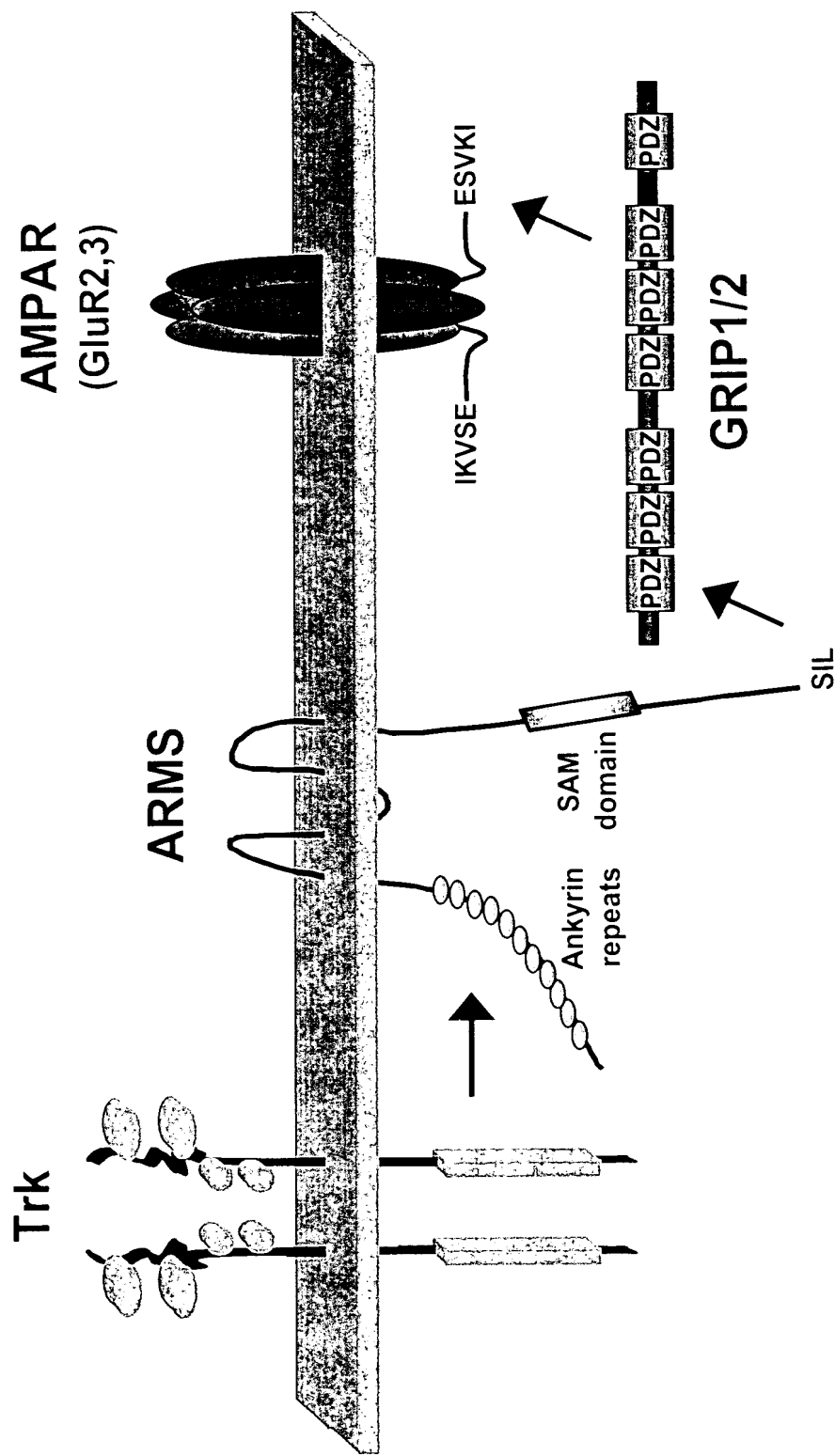


FIG. 20